

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2001, 10:52:56 ; Search time 30.06 Seconds
(without alignments)
33.883 Million cell updates/sec

Title: US-09-288-719-3

Perfect score: 81

Sequence: 1 GGGGSGGRASGGGS 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	233	2 JC5322	p53 specific singl
2	68	84.0	268	2 A56446	Ig heavy chain V r
3	67	82.7	586	2 T26667	hypothetical prote
4	67	82.7	877	2 T43449	hypothetical prote
5	67	82.7	1433	2 A46053	bullous pemphigoid
6	66	81.5	592	2 E82759	end-1,4-beta-gluc
7	66	81.5	779	2 A35006	cell surface glyco
8	65	81.5	1585	2 T31611	hypothetical prote
9	65	80.2	104	2 JC4190	holotricin 3 precu
10	65	80.2	136	2 T29282	hypothetical prote
11	65	80.2	221	2 T04592	glycine-rich cell
12	65	80.2	316	2 T20497	hypothetical prote
13	65	80.2	643	1 KRHU2	keratin 1, type II
14	64	79.0	249	2 S41374	single chain Fv an
15	63	77.8	206	2 T53066	gene M-twist prote
16	63	77.8	214	1 KNNP25	glycine-rich prote
17	63	77.8	239	2 S49193	GCR 101 protein -
18	63	77.8	265	2 A40649	hypothetical prote
19	63	77.8	271	2 S34666	glycine-rich prote
20	63	77.8	312	2 T25048	hypothetical prote
21	63	77.8	431	1 WTHU2G	homeotic protein H
22	63	77.8	433	2 S20963	homeotic protein H
23	63	77.8	1454	2 T13709	diacylglycerol kin
24	62	76.5	80	2 T10550	hypothetical prote
25	62	76.5	157	1 S14857	glycine-rich prote
26	62	76.5	157	1 S04536	embryonic abundant
27	62	76.5	165	1 KNR2G1	glycine-rich cell
28	62	76.5	168	1 S12312	glycine-rich RNA-b
29	62	76.5	207	2 T07381	glycine-rich prote

30	62	76.5	280	2 A42424	chitinase (EC 3.2.
31	62	76.5	291	1 S31415	glycine-rich prote
32	62	76.5	322	2 A45036	single-stranded-DN
33	62	76.5	333	2 S16318	homeotic protein H
34	62	76.5	378	2 S04336	U1 snRNP 70K prote
35	62	76.5	440	2 S71795	transcription fact
36	62	76.5	495	1 S31223	transcription fact
37	62	76.5	528	2 G02127	transcription fact
38	62	76.5	569	1 KRMS1	fus-like protein -
39	62	76.5	570	2 S07330	keratin, 59K type
40	62	76.5	979	2 A35913	regulatory factor
41	62	76.5	1969	2 T08875	histidine kinase h
42	62	76.5	2783	1 A41948	alpha-fetoprotein
43	61	75.3	102	2 D71415	hypothetical prote
44	61	75.3	165	2 T03583	glycine-rich RNA-b
45	61	75.3	316	1 A38743	loricrin - human

ALIGNMENTS

RESULT 1
JC5322
p53 specific single-chain antibody Pab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Janot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; M01D:97168950
A:Accession: JC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JN>
A:Experimental source: hybridoma cell
C:Comment: this protein specifically binds the tumor suppressor protein p53. It resto

Query Match 100.0%; Score 81; DB 2; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGSGGRASGGGS 15
DB 110 GGGGSGGRASGGGS 124

RESULT 2

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ide

A:Reference number: A56446; M01D:95229583
A:Accession: A56446

A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-268 <TN>
A:Cross-references: GB:U20617

C:Keywords: heterotrimer; immunoglobulin

Query Match 84.0%; Score 68; DB 2; Length 268;
Best Local Similarity 86.7%; Pred. No. 0.53;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGGSGGRASGGGS 15
DB 121 GGGGSGGRASGGGS 135

RESULT 3
726667
hypothetical protein Y38E10A.g - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26667
R:Wallis, J.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20252

A:Accession: T26667

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-586 <MIT>

A:Cross-references: EMBL:AL110484; NID:e1542205; PIDN:CAB54408.1; CESP:Y38E10A.g

A:Experimental source: clone Y38E10A

C:Genetics:

A:Gene: CESP:Y38E10A.g

A:Introns: 105/2; 174/1; 248/1; 372/3; 436/3

Query Match 82.7%; Score 67; DB 2; Length 586;
Best Local Similarity 80.0%; Pred. No. 1.3;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGGGS 15
||||||| :|||||
Db 461 GGGGSGGYCAGGCGGS 475

RESULT 4

T43449
hypothetical protein DKFZP434P0917.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T43449

R:Boecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, December 1999

A:Reference number: Z22513

A:Accession: T43449

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-877 <AA>

A:Cross-references: EMBL:AL133612

A:Experimental source: adult testis; clone DKFZP434P0917

C:Genetics:

A:Note: DKFZP434P0917.1

Query Match 82.7%; Score 67; DB 2; Length 877;
Best Local Similarity 80.0%; Pred. No. 1.8;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGGGS 15
||||| :|||||
Db 143 GGGGSGGSSGGGGS 157

RESULT 5

A46053
bullous pemphigoid antigen, BPAG2, type XVII collagen alpha 1-chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-Sep-1993 #sequence_revision 21-Sep-1993 #text_change 05-Nov-1999

C:Accession: A46053

R:Li, K.; Tamai, K.; Tan, E.M.L.; Uitto, J.

J Biol. Chem. 268; 8825-8834, 1993

A:Title: Cloning of type XVII collagen. Complementary and genomic DNA sequences of mouse

egment, and unusual features in the 5'-end of the gene and the 3'-untranslated region of

A:Reference number: A46053

A:Accession: A46053

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1433 <L11>

A:Cross-references: GB:L08407; NID:g309182; PIDN:AAA37443.1; PID:g309183
A:Note: sequence extracted from NCBI backbone (NCBIN:129627, NCBI:P:129628)

Query Match 82.7%; Score 67; DB 2; Length 1433;
Best Local Similarity 80.0%; Pred. No. 2.8;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGGGS 15
||||| :|||||
Db 443 GGGGSGGASGGGGA 457

RESULT 6

E82759
endo-1,4-beta-glucanase XF0818 (imported) - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: E82759

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: E82759

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-592 <SIM>

A:Cross-references: GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83628.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alverenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carr

as-Neto, E.; Docena, C.; El-Porcy, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmetti,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0818

Query Match 81.5%; Score 66; DB 2; Length 592;
Best Local Similarity 85.7%; Pred. No. 1.7;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGGGS 14
||||||| :|||||
Db 467 GGGGSGGSGGGGGG 480

RESULT 7

A35006
cell surface glycoprotein msp130 precursor - sea urchin (Strongylocentrotus purpuratu

C:Species: Strongylocentrotus purpuratus (purple urchin)

C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Sep-1997

C:Accession: A35006; A45939

R:Part, B.A.; Parks, A.L.; Raff, R.A.

J Biol. Chem. 265; 1408-1413, 1990

A:Title: Promoter structure and protein sequence of msp130, a lipid-anchored sea urch

A:Reference number: A35006; MUID:90110195

A:Accession: A35006

A:Status: preliminary

A:Molecule type: DNA; mRNA

A:Residues: 1-779 <PAR>

A:Cross-references: GB:M31751; NID:g161543; PID:g161544; GB:J05204

R:Leat, D.S.; Anstrom, J.A.; Chin, J.E.; Harkey, M.A.; Snowman, R.M.; Raff, R.A.

Dev. Biol. 121, 29-40, 1987
A:Title: Antibodies to a fusion protein identify a cDNA clone encoding msp130, a primary

A:Reference number: A45939; MID:87191419

A:Accession: A45939

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 542-779 <LEA>

A:Cross-references: GB:M16457; MID:g161539; PID:g161540

C:Keywords: glycoprotein

Query Match

Best Local Similarity 81.5%; Score 66; DB 2; Length 779;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGCG 14
||||| ||| ||| |||
Db 57 GGGGAGRGGGGGG 70

RESULT 8

TJ1611

hypothetical protein Y508A.g - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: TJ1611

R:Steward, C. submitted to the EMBL Data Library, September 1999

A:Reference number: Z21047

A:Accession: TJ1611

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1585 <MTL>

A:Cross-references: EMBL:AL117200; MID:e1549770; PID:CAE55050.1; CESP:Y508A.g

A:Experimental source: clone Y508A

C:Genetics:

A:Gene: CESP:Y508A.g

A:Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2

Query Match

Best Local Similarity 81.5%; Score 66; DB 2; Length 1585;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGCG 14
||||| ||| ||| |||
Db 452 GGGGCGGAGGCGG 465

RESULT 9

JC4190

holotricin 3 precursor - Holotrichia diomphalia

N:Alternate names: antifungal protein

C:Species: Holotrichia diomphalia

C:Date: 04-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: JC4190

R:Lee, S.Y.; Moon, H.J.; Kurata, S.; Natori, S.; Lee, B.L.

Biol. Pharm. Bull. 18, 1049-1052, 1995

A:Title: Purification and cDNA cloning of an antifungal protein from the hemolymph of Hc

A:Reference number: JC4190; MID:96073722

A:Accession: JC4190

A:Molecule type: mRNA

A:Residues: 1-104 <LEA>

A:Cross-references: DBJ:D13744; MID:g1088433; PIDN:BAA02889.1; PID:di003394; PID:g17861

C:Comment: This protein is a Gly- and His-rich protein and a constitutive protein of lat

C:Keywords: hemolymph

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-104/Product: holotricin 3 #status predicted <MAT>

Query Match

Best Local Similarity 80.2%; Score 65; DB 2; Length 104;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGGS 15
||||| ||| ||| |||
Db 64 GGGRRGGGGSGGGS 78

RESULT 10

T29282

hypothetical protein C34D4.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T29282

R:Du, Z.; Lee, T.F.

submitted to the EMBL Data Library, May 1996

A:Description: The sequence of C. elegans cosmid C34D4.

A:Reference number: Z20500

A:Accession: T29282

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-136 <DUZ>

A:Cross-references: EMBL:U58755; PIDN:AB00696.1; GSPDB:GN00022; CESP:C34D4.11

A:Experimental source: strain Bristol N2; clone C34D4

C:Genetics:

A:Gene: CESP:C34D4.11

A:Map position: 4

A:Introns: 20/1; 66/1; 98/1; 116/1

C:Superfamily: Arabidopsis glycine-rich protein 3

Query Match

Best Local Similarity 80.2%; Score 65; DB 2; Length 136;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGCG 14
||||| ||| ||| |||
Db 97 GGGGCGGRRGGGCG 110

RESULT 11

T04592

glycine-rich cell wall structural protein homolog F23E13.120 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999

C:Accession: T04592

R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse,

submitted to the Protein Sequence Database, March 1998

A:Reference number: Z15378

A:Accession: T04592

A:Molecule type: DNA

A:Residues: 1-221 <BEV>

A:Cross-references: EMBL:AL022141

C:Experimental source: cultivar Columbia; BAC clone F23E13

C:Genetics:

A:Map position: 4

A:Note: F23E13.120

Query Match

Best Local Similarity 80.2%; Score 65; DB 2; Length 221;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GGGGSGGRASGGCG 14
||||| ||| ||| |||
Db 98 GGGGCGGSGGGGCG 111

RESULT 12

T20497

hypothetical protein F02D10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T20497

R:Swirnburne, J.

A: Introns: 56/3

DD 98 GGGGGGEEAAAGGG 111

RESULT 13

KRH02

keratin 1, type II, cytoskeletal - human

N:Alternate names: 67K type II epidermal keratin; cytokeratin 1

C:Species: Homo sapiens (man)

C:Date: 04-Dec-1986 #sequence_revision 22-Oct-1999 #text_change 10-Dec-1999

C:Accession: A22940; A02950; A43342

R:Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985

A:Reference number: A22940; MUID:85166239

A:Accession: A22940

A:Molecule type: DNA

A:Residues: 1-643 <JOH>

A:Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:g1843461

A>Note: translation of Initiator Met is not shown

R:Steinert, P.M.; Perry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.

J. Biol. Chem. 260, 7142-7149, 1985

A:Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000

late filament subunits.

A:Reference number: A92535; MUID:85207740

A:Accession: A02950

A:Molecule type: mRNA

A:Residues: 1-183, 'K', 185-199, 'M', 201-204, 'K', 206-236, 'S', 238-239, 'R', 241-356, 'Y', 358-

'S', 638-643 <STE>

A:Cross-references: GB:M10938; NID:g186787; PIDN:AA36153.1; PID:g386854

A:Experimental source: tissue neonatal foreskin

A>Note: the authors translated the codon CUG for residue 476 as Met

R:Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; Digiovanna, J.J.; Compton, J.G.; S

Cell 70, 821-828, 1992

A:Title: A leucine----proline mutation in the H1 subdomain of keratin 1 causes epidermol

A:Reference number: A43342; MUID:92386601

A:Accession: A43342

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHT>

A:Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:g1843461

A>Note: sequence extracted from NCBI backbone (NCBI:P113784)

C:Comment: The cytoskeletal and microfibrillar keratins are classified into two types, t

atin if protein subunit appears to be a heterotetramer of two type I and two type II prot

C:Comment: Keratin 1 is expressed in terminally differentiating epidermis.

C:Genetics:

A:Gene: GDB:KRT1

A:Cross-references: GDB:128198; OMIM:139350

A:Map position: 12q11-12q13

A>Note: defects in this gene may result in epidermolytic hyperkeratosis

C:Complex: heterotetramer of two type I, usually keratin 10 (see PIR:KRH00), and two ty

C:Superfamily: cytoskeletal keratin

C:Keywords: coiled coil; heterotetramer; intermediate filament

F:4-19/Domains: head <HBD>

```

F: 4-143/Region: E1 and V1 subdomains
F: 1-179/Region: H1 subdomain
F: 180-492/Domain: rod <ROD>
F: 180-214/Region: coil 1A
F: 215-226/Region: linker 1
F: 227-327/Region: coil 1B
F: 328-344/Region: linker 12
F: 345-363/Region: coil 2A
F: 364-371/Region: linker 2
F: 372-492/Region: coil 2B
F: 430/Region: stutter
F: 493-643/Domain: tail <END>
F: 493-512/Region: H2 subdomain
F: 513-643/Region: V2 and E2 subdomains

```

	Query Match	80.2%	Score 65	DB 1	Length 643
	Best Local Similarity	80.0%	Pred. No. 2.3		
	Matches 12	Conservative 0	Mismatches 3	Indels 0	Gaps 0
QY	1 GGGGSGRAGGGGS	15			
db	594 GGGSSGGRSGGGSS	608			

RESULT 14
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library January 1994
A:Description: Construction and functional characterization of a single chain Fv anti-
A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

	Query Match	Best Local Similarity	Matches	Score	Pred. No.	DB	Length	Mismatches	Indels	Gaps
QY	2	GGGSGGRASGGGS	15	79.03	64	249				
Db	121	GGGSGGGGSGGGGS	134	85.78	1	4		0	2	0

RESULT 15
153066
gene M-twist protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: 153066; 166795
R:Wolf, C.; Thisse, C.; Stoetzel, C.; Thisse, B.; Gerlinger, P.; Perrin-Schmitt, F.
Dev. Biol. 143, 365-373, 1991
A:Title: The M-twist gene of Mus is expressed in subsets of mesodermal cells and its
A:Reference number: 153066; MUID:91122450
A:Accession: 153066
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-206 <RES>
A:Cross-References: GB:M63649; NID:9202243; PIDN:AAA40514.1; PID:9202244
A:Accession: 166795
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-35, 'R', '37-90', 'P', '92-206 <RES>
A:Cross-References: GB:M63650; NID:9202245; PIDN:AAA40515.1; PID:9202246
C:Genetics:
A:Gene: M-twist

Query Match 77.8%; Score 63; DB 2; Length 206;
Best Local Similarity 73.3%; Pred. No 1.5;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGSGGRASGGGS 15
|||||
Db 83 GGGGAGGGGGGGGS 97

Search completed: March 15, 2001, 10:52:57
job time: 1006 sec